RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/659,737A

DATE: 02/26/2002
TIME: 13:59:19

Input Set : A:\71369-172(PFI-024US).ST25.txt
Output Set: N:\CRF3\02262002\I659737A.raw


```
  3 <110> APPLICANT: Blumenberg, Miroslav
  4       Gazel, Alix M.
  6 <120> TITLE OF INVENTION: Genes and Polynucleotides Associated with Ultraviolet
  7       Radiation-Mediated Skin Damage and Uses Thereof
  9 <130> FILE REFERENCE: 71369.172(PFI-024US)
 11 <140> CURRENT APPLICATION NUMBER: US 09/659,737A
 12 <141> CURRENT FILING DATE: 2000-09-11
 14 <150> PRIOR APPLICATION NUMBER: US 60/155,029
 15 <151> PRIOR FILING DATE: 1999-09-20
 17 <160> NUMBER OF SEQ ID NOS: 19
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 164
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (2)...(163)
 30 <400> SEQUENCE: 1
 31 g cac cgg gac atc aag gca gga aat att ttg cta ctt gag aag ata gaa 49
 32   His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Leu Glu Lys Ile Glu
 33    1               5                  10                  15
 35 cat gat gac atc tgc aat aaa act ttg aag att aca gat ttt ggg ttg   97
 36 His Asp Asp Ile Cys Asn Lys Thr Leu Lys Ile Thr Asp Phe Gly Leu
 37             20                  25                  30
 39 gcg agg gaa tgg cac agg acc acc aaa atg agc aca gca ggc acc tat   145
 40 Ala Arg Glu Trp His Arg Thr Thr Lys Met Ser Thr Ala Gly Thr Tyr
 41          35                  40                  45
 43 gcc tgg atg gcc cca gaa g                                       164
 44 Ala Trp Met Ala Pro Glu
 45       50
 48 <210> SEQ ID NO: 2
 49 <211> LENGTH: 54
 50 <212> TYPE: PRT
 51 <213> ORGANISM: Homo sapiens
 53 <400> SEQUENCE: 2
 54 His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Leu Glu Lys Ile Glu
 55  1               5                  10                  15
 56 His Asp Asp Ile Cys Asn Lys Thr Leu Lys Ile Thr Asp Phe Gly Leu
 57             20                  25                  30
 58 Ala Arg Glu Trp His Arg Thr Thr Lys Met Ser Thr Ala Gly Thr Tyr
 59          35                  40                  45
 60 Ala Trp Met Ala Pro Glu
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61     50
64 <210> SEQ ID NO: 3
65 <211> LENGTH: 145
66 <212> TYPE: DNA
67 <213> ORGANISM: Homo sapiens
69 <220> FEATURE:
70 <221> NAME/KEY: CDS
71 <222> LOCATION: (2)...(145)
73 <400> SEQUENCE: 3
74 a cat cgg gac atc aag agc gac tcg atc ctg ctg acc cat gat ggc agg 49
75   His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr His Asp Gly Arg
76    1               5                  10                  15
78 gtg aag ctg tca gac ttt ggg ttc tgc gcc cag gtg agc aag gaa gtg   97
79 Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Val Ser Lys Glu Val
80              20                  25                  30
82 ccc cga agg aag tcg ctg gtc ggc acg ccc tac tgg atg gcc cca gag   145
83 Pro Arg Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
84          35                  40                  45
88 <210> SEQ ID NO: 4
89 <211> LENGTH: 48
90 <212> TYPE: PRT
91 <213> ORGANISM: Homo sapiens
93 <400> SEQUENCE: 4
94 His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr His Asp Gly Arg
95  1               5                  10                  15
96 Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Val Ser Lys Glu Val
97             20                  25                  30
98 Pro Arg Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
99         35                  40                  45
102 <210> SEQ ID NO: 5
103 <211> LENGTH: 146
104 <212> TYPE: DNA
105 <213> ORGANISM: Homo sapiens
107 <220> FEATURE:
108 <221> NAME/KEY: CDS
109 <222> LOCATION: (2)...(145)
111 <400> SEQUENCE: 5
112 t cac agg gac atc aag agt gac tcc atc ctg ctg acc ctc gat ggc agg 49
113   His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr Leu Asp Gly Arg
114    1               5                  10                  15
116 gtg aag ctc tcg gac ttc gga ttc tgt gct cag atc agc aaa gac gtc   97
117 Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Ile Ser Lys Asp Val
118             20                  25                  30
120 cct aag agg aag tcc ctg gtg gga acc ccc tac tgg atg gcg ccc gag   145
121 Pro Lys Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
122          35                  40                  45
124 g                                                               146
126 <210> SEQ ID NO: 6
127 <211> LENGTH: 48
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<SEQ_TYPE_PRT>
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 6

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His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr Leu Asp Gly Arg
 1               5                  10                  15
Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Ile Ser Lys Asp Val
            20                  25                  30
Pro Lys Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
        35                  40                  45
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<SEQ_TYPE_DNA>
<210> SEQ ID NO: 7
<211> LENGTH: 3627
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (868)..(1275)
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1420)..(1553)
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1900)..(2026)
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (2105)..(2230)
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (2696)..(2833)
<400> SEQUENCE: 7

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agagccaaaa gagaacatga cggccctgca ctccgggatc tctctggcac cagattccca    120
gcccagggga gacacctgaa ccccccagat ggtgacacac ctctgtggtc ctctgtcagg    180
gacataacct cccagcacag atttgcaaac tccctgctgc aggcacaagc agggctatcg    240
ggccccaggt gtggctcccc tgccttggtt cagggagtgg agacacagtt gcccactgct    300
ccccacccca ctgccaggcc tcttctgccc ccatgggtcc tggggtgggg gagccttggg    360
agttgaagaa tgcctctgac ccagattctt caagcagcct ctgagctcag aggaagagtc    420
tgcctcacgg cagcctccct ggggtctagc tgtcaatcgc ccaggaagaa atacccagcg    480
cgggacccgg cggggaagct ggccttctct gtcttcccag gtgcagcaca gcgagtgtaa    540
ggagctgtct tgggcctgcc cagcctggtg ccctgcgggg gactgctggc acaggactgt    600
gactgggctt cagctctgtc tgaaaatctt tgcttcagag cacctcccta gtttgatctg    660
ataccccgcc tgaccctgcc agagtccaga ggtcacggcg gccagccccc gcctccggga    720
aggttattcc aaatgctccc acagccctga cccttcctgt tgctttgtcc cttgcagccc    780
aactcctctt tccgaccgcc gcagaaagac aacccccaa gcctggtggc caaggcccag     840
tccttgccct cggaccagcc ggtgggg acc ttc agc cct ctg acc act tcg gat    894
                              Thr Phe Ser Pro Leu Thr Thr Ser Asp
                              1               5
acc agc agc ccc cag aag tcc ctc cgc aca gcc ccg gcc aca ggc cag      942
Thr Ser Ser Pro Gln Lys Ser Leu Arg Thr Ala Pro Ala Thr Gly Gln
10                  15                  20                  25
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```
188 ctt cca ggc cgg tct tcc cca gcg gga tcc ccc cgc acc tgg cac gcc      990
189 Leu Pro Gly Arg Ser Ser Pro Ala Gly Ser Pro Arg Thr Trp His Ala
190                 30                  35                  40
192 cag atc agc acc agc aac ctg tac ctg ccc cag gac ccc acg gtt gcc     1038
193 Gln Ile Ser Thr Ser Asn Leu Tyr Leu Pro Gln Asp Pro Thr Val Ala
194             45                  50                  55
196 aag ggt gcc ctg gct ggt gag gac aca ggt gtt gtg aca cat gag cag     1086
197 Lys Gly Ala Leu Ala Gly Glu Asp Thr Gly Val Val Thr His Glu Gln
198         60                  65                  70
200 ttc aag gct gcg ctc agg atg gtg gtg gac cag ggt gac ccc cgg ctg     1134
201 Phe Lys Ala Ala Leu Arg Met Val Val Asp Gln Gly Asp Pro Arg Leu
202     75                  80                  85
204 ctg ctg gac agc tac gtg aag att ggc gag ggc tcc acc ggc atc gtc     1182
205 Leu Leu Asp Ser Tyr Val Lys Ile Gly Glu Gly Ser Thr Gly Ile Val
206 90                  95                  100                 105
208 tgc ttg gcc cgg gaa gaa cac tcg ggc cgc cag gtg gcc gtc aag atg     1230
209 Cys Leu Ala Arg Glu Glu His Ser Gly Arg Gln Val Ala Val Lys Met
210                 110                 115                 120
212 atg gac ctc aga aag cag cag cgc agg gag ctg ctc ttc aac gag         1275
213 Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu
214             125                 130                 135
216 gtgggaggac agggtgggac acacacgggg gcgttgggga tgggcagtga gcagccagcc   1335
217 aggctggaca tctgtgagca ggggcagtgg gtggccatgc gtctgggcac tgtgcctggc   1395
218 actcaggccc ccacctgccc ccag gtg gtg atc atg cgg gac tac cag cac      1446
219                             Val Val Ile Met Arg Asp Tyr Gln His
220                                 140                 145
222 ttc aac gtg gtg gag atg tac aag agc tac ctg gtg ggc gag gag ctg     1494
223 Phe Asn Val Val Glu Met Tyr Lys Ser Tyr Leu Val Gly Glu Glu Leu
224                 150                 155                 160
226 tgg gtg ctc atg gag ttc ctg cag gga gga gcc ctc aca gac atc gtc     1542
227 Trp Val Leu Met Glu Phe Leu Gln Gly Gly Ala Leu Thr Asp Ile Val
228             165                 170                 175
230 tcc caa gtc ag  gtgggcagct gggagggctg gaccctgagt gcaggctgcc         1593
231 Ser Gln Val Arg
232         180
234 ctcaccatgg ccctgccagg gcaatgtggt cttctgcctg tggcccagaa gacttgggat   1653
235 gcctgggctc ccctgcctgc tggggtaact gagacccagg ggtcttggga gtggagaaga   1713
236 gaaggatagc ttctagccaa agctcaggcc ccagttttca ccagggctat ggcctgactg   1773
237 tgctgccaaa cagattgcct gggagctgtg gggcctagca ccagggactc ctactctgct   1833
238 cagccacccc acgacctgcc agagctaacg ttctctttca tcgggtggcc ccaccttcct   1893
239 gtccag g ctg aat gag gag cag att gcc act gtg tgt gag gct gtg ctg     1942
240          Leu Asn Glu Glu Gln Ile Ala Thr Val Cys Glu Ala Val Leu
241                     185                 190                 195
243 cag gcc ctg gcc tac ctg cat gct cag ggt gtc atc cac cgg gac atc     1990
244 Gln Ala Leu Ala Tyr Leu His Ala Gln Gly Val Ile His Arg Asp Ile
245                 200                 205                 210
247 aag agt gac tcc atc ctg ctg acc ctc gat ggc agg gtaggtccca         2036
248 Lys Ser Asp Ser Ile Leu Leu Thr Leu Asp Gly Arg
249             215                 220
```

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```
251 tcctgtccct ggcacagcca cgctcccact tcctcctgat ccaccactca ctccctttc   2096
252 aaccgcag gtg aag ctc tcg gac ttc gga ttc tgt gct cag atc agc aaa    2146
253          Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Ile Ser Lys
254              225                 230                 235
256 gac gtc cct aag agg aag tcc ctg gtg gga acc ccc tac tgg atg gct    2194
257 Asp Val Pro Lys Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala
258          240                 245                 250
260 cct gaa gtg atc tcc agg tct ttg tat gcc act gag gtaaccgttc         2240
261 Pro Glu Val Ile Ser Arg Ser Leu Tyr Ala Thr Glu
262      255                 260                 265
264 cctccacccc ccagacctcc caaaagcaac ttggcaactg gcagctcttc tgctgtggcc  2300
265 cctccagtga gctcaccaaa agcagccctg gttttcagag tcccacctag tcaacaccct  2360
266 tccccctttc gatggggctg ctcttaccca gtgactttgc tgccaggaac gagtcctgca  2420
267 agtgctttcc tcagctcaag ggcagaatgg ggtatggccg ggcctcctat gtatgatggc  2480
268 ctttctctga gtgactgaca gctgtgtccc tataggcagt ggtcactcat gcaggcagta  2540
269 actggccaca gggcaggtga ccaggggagg aaggagacag acccaccaag gagagctggg  2600
270 gccagctgtc ccccctccac cactgctgcc accagaacgc agctaccaat gggccagggt  2660
271 ctggccatgg ggtcagggac attttcctcc tgcag gtg gat atc tgg tct ctg      2713
272                                     Val Asp Ile Trp Ser Leu
273                                                 270
275 ggg atc atg gtg att gag atg gta gat ggg gag cca ccg tac ttc agt      2761
276 Gly Ile Met Val Ile Glu Met Val Asp Gly Glu Pro Pro Tyr Phe Ser
277              275                 280                 285
279 gac tcc cca gtg caa gcc atg aag agg ctc cgg gac agc ccc cca ccc     2809
280 Asp Ser Pro Val Gln Ala Met Lys Arg Leu Arg Asp Ser Pro Pro Pro
281          290                 295                 300
283 aag ctg aaa aac tct cac aag gtc agttggcaca caagggtgcg acctcgcaga    2863
284 Lys Leu Lys Asn Ser His Lys Val
285      305                 310
287 ccccattcct cctgaggcaa ggggaccaga acctgggctc ccagcatctc ccttccactg  2923
288 aagccacagg gtctgggctc ctggaaaagg ctcctctttc cccacacaaa acccgcacct  2983
289 gggtgtggag ccgcatctac gcacaagttc gcatgtcgcc tccgacaagt cgcctcccac  3043
290 ggctgtggca ggagagttgc tgcttggcag aagggttgct gcttggcagg cactggtcgg  3103
291 aagcccagtg gggcccatga gcagggaaag ccaggacacc agcaactccc tgctgtccag  3163
292 ggagggatcc ggagaagctt cactgagcac aaacccttca acccgtgtcg ggagatccat  3223
293 accatgattc gatgtccctg tccatcacgg cgagtcggct catgctccat tcgttgcaca  3283
294 ccccgacaca gctaagccac agcgttcccc ttaaagccag tataagtgca tggaagtggt  3343
295 atacatgtaa ccctttttgc caaatcggcc ccaaccccgc aggccttact gtggacgccc  3403
296 cctgctggca ggtcagcacg gggctgataa gtggcaccgc catctggtgg ccaaaacaag  3463
297 aaatgtctca gagggctgaa gcctctcctc taaaatagca aaaaaacaag agttctgtgg  3523
298 ccccaacaca aagctggatg ggaggaccaa caggaaacat cttccaagac aactggtcct  3583
299 tggagcccgc accgctaacc ccaaaattag catataaagc atgc                   3627
302 <210> SEQ ID NO: 8
303 <211> LENGTH: 311
304 <212> TYPE: PRT
305 <213> ORGANISM: Homo sapiens
307 <400> SEQUENCE: 8
308 Thr Phe Ser Pro Leu Thr Thr Ser Asp Thr Ser Ser Pro Gln Lys Ser
309 1               5                  10                  15
```

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/659,737A

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Input Set : A:\71369-172(PFI-024US).ST25.txt
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L:660 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1021 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1047 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1060 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17